

MRLEGPGLSLLCLVLALPALLPVPAVRGVAETPTYWPRDAETGERLVCAQCPPGTFVQR
PCRRDSPPTCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTPSQNTQCQPCPPGTFSASSSSSEQCQPHRNCTALGLA
LNVPGSSSHDTLCTSGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLALEAPE
GWGPTPRAGRAALQLKLRRRLTELLGAQDGALLVRLQLRVARMPGLERSVRERFLPVH

Fig. 1

TCCGCAGGCGGACCGGGGCAAAGGAGGTGGCATGTGCGTCAGGCACAGCAGGGTCCTGT
GTCCGCGCTGAGCCGCGCTCTCCCTGCTCCAGCAAGGACC
><Met (trans=1-s, dir=f, res=1)>
ATGAGGGCGCTGGAGGGGCCAGGCCTGTCGCTGCTGTGCCTGGTGTGGCGCTGCCTGCC
CTGCTGCCGGTGCCGGCTGTACGCGGAGTGGCAGAAACACCCACCTACCCCTGGCGGGAC
GCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCGCGGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCTGCGCTGCCGACCGGCTTCTTC
GCGCACGCTGGTTTCTGCTTGAGCACGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
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CTCAGCACCAGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGAG
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCTTGCAGCTGAAGCTGCGTCGGCGG
CTCAGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGGGCTGCTGCAGGCGCTG
CGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC
TGATCCTGGCCCCCTTTATTTATTCTACATCCTTGGCACCCCACTTGCACTGAAAGAGG
CTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTGGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCAGCCA
GAACACGCAGTGCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCAGGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

Fig. 3

SEQ ID NO: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 6 1
 SEQ ID NO: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 G
 SEQ ID NO: 4 178 CA-TTCTGGAACCTGGAGCGC
 SEQ ID NO: 5 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNGG
 SEQ ID NO: 6 2 CAGTTCTGGAACCTACTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
 SEQ ID NO: 3 51 CAGTTCTGGAANTAACTGGAGCNCCTGCCGCTACTGNAACGTCCTCTGNGG
 SEQ ID NO: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
 SEQ ID NO: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
 SEQ ID NO: 7 1 GAGGGCCCCCAGGAGTGCTGCGCACCCACAACCGTGCCT
 SEQ ID NO: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
 SEQ ID NO: 5 151 GCNGCTGCAGCACCGGNTTCTTCGGCAGCGTGNTTCTGCTTGGAGCAC
 SEQ ID NO: 6 102 GCCGCTGCCGACACCGGCTTCTTCGGCAGCGTGTTCTGCTTGGAGCAC
 SEQ ID NO: 7 32 TGGCAGGGGTCAGGTTGCTGTGCCAGCCTTGCAACCTGAGCTAGGACAC
 SEQ ID NO: 3 151 GCCGCTGCCGACCGGCTTCTTCGGCAGCGTGTTCTGCTTGGAGCAC
 SEQ ID NO: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
 SEQ ID NO: 6 152 GCATCGTGTCCACCTGGTGC CGCGGTGATTNCCCCGGGCACCCCCAGCCA
 SEQ ID NO: 7 82 CAGTTCCCCCTGACCCCTGTTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
 SEQ ID NO: 8 1 GCATCGTGTCCACCTGGTGC CGCGGTGATTGCCCCGGGCACCCCCAGCCA
 SEQ ID NO: 10 1 CTTGTCCACCTGGTGC CGCGGTGATTNCCC-GGGCACCCCCAGCCA
 SEQ ID NO: 3 201 GCATCGTGTCCACCTGGTGC CGCGGTGATTGCCCCGGGCACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA-TGCAAAAGCCGTG
 SEQ ID NO: 7 132 GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 8 51 GAACACGCAG-GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 10 47 GAACACGCAGTGC-AGCCT-CCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 9 1 AGCNGTGCNCCNAGGCACCTTCTCAGCCAGCAGT
 SEQ ID NO: 3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAG
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCCAGCT
 SEQ ID NO: 10 197 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 10 247 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 9 186 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT
 SEQ ID NO: 3 451 CGTGCCGTCATCGACTTTGTGGCTTCCAGGACATCTCCAT

Fig. 4 (cont.)

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P 25

CRD1

DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62
 OPG 26 - . P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93
 OPG 55 T A K W K T V C A P C P D H Y T D S W H T S D E C L Y C S P 85

CRD2

DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4

DcR3 156 G T F S A S S S S S E Q C Q P H R N C T A L G L A L N V P G S 186
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T . P R 247
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L . L V R L L 277
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

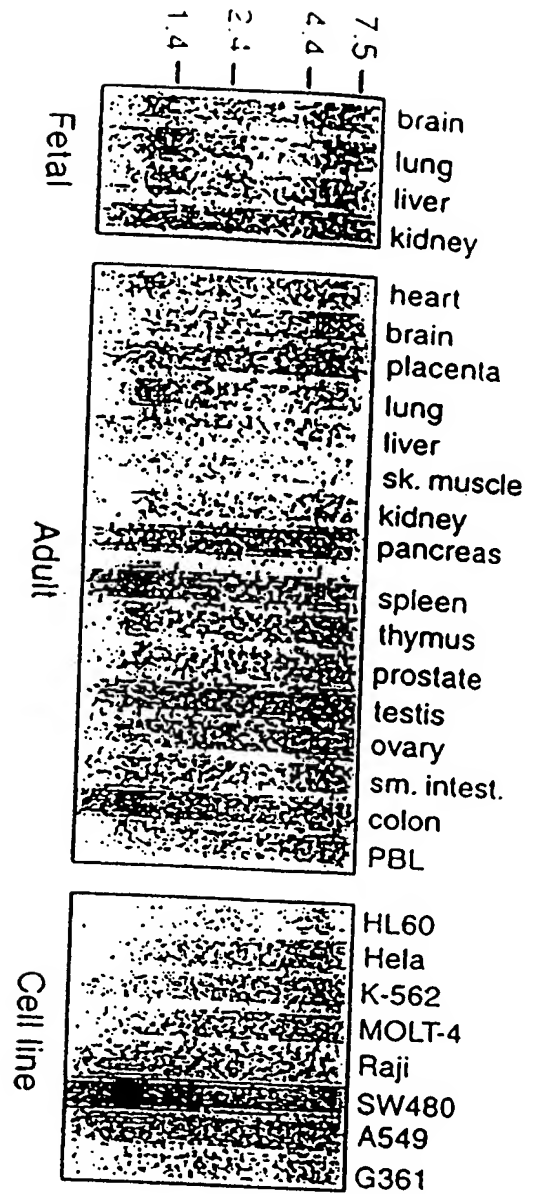


Fig. 7

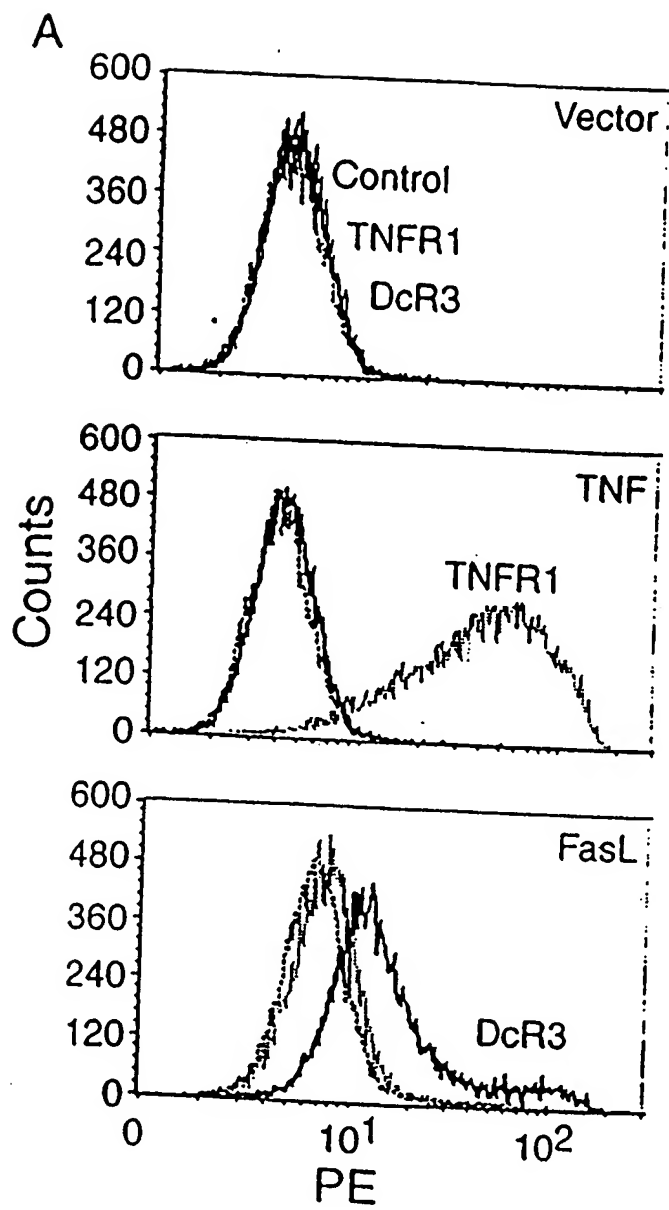
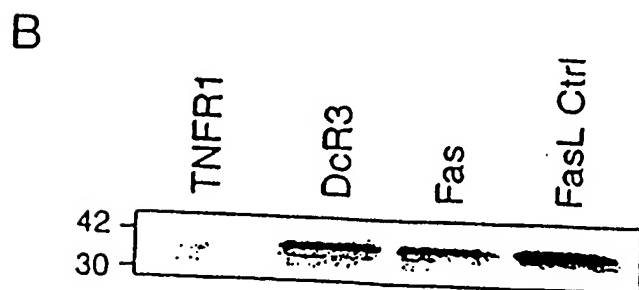


Fig. 8



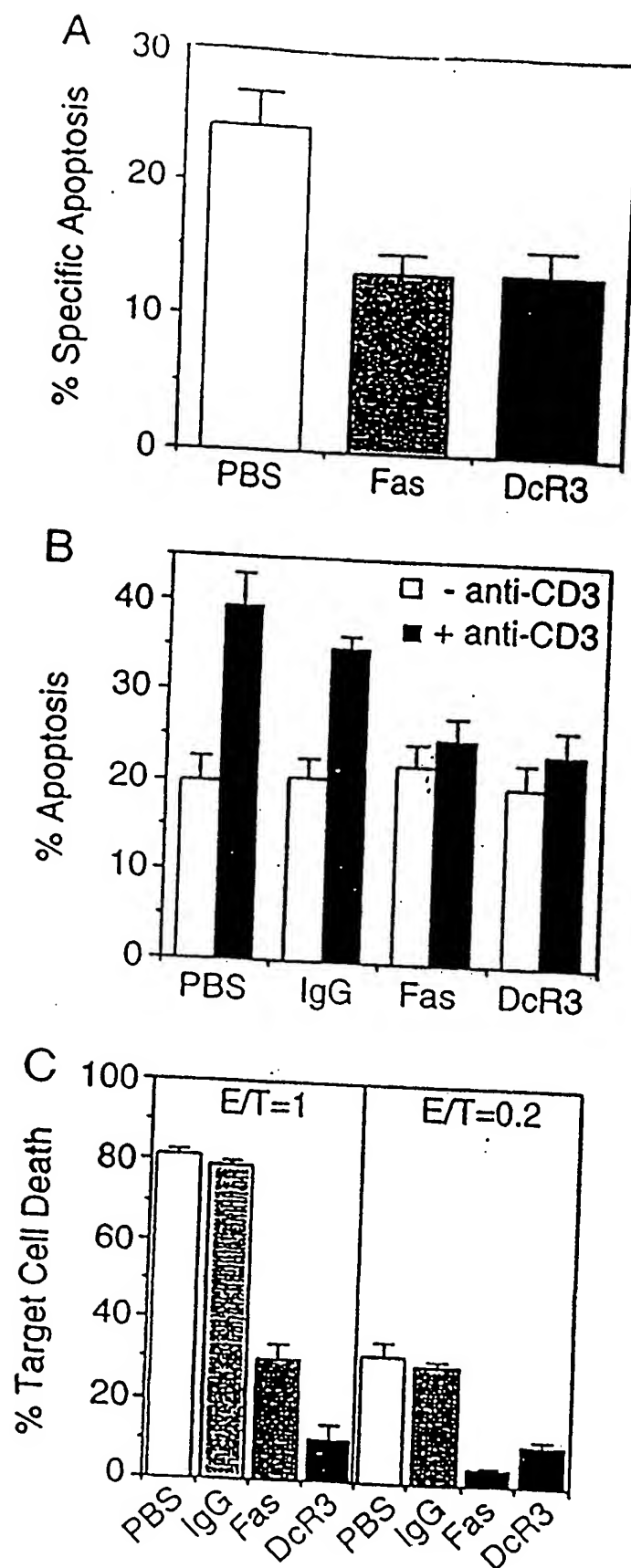


Fig. 9

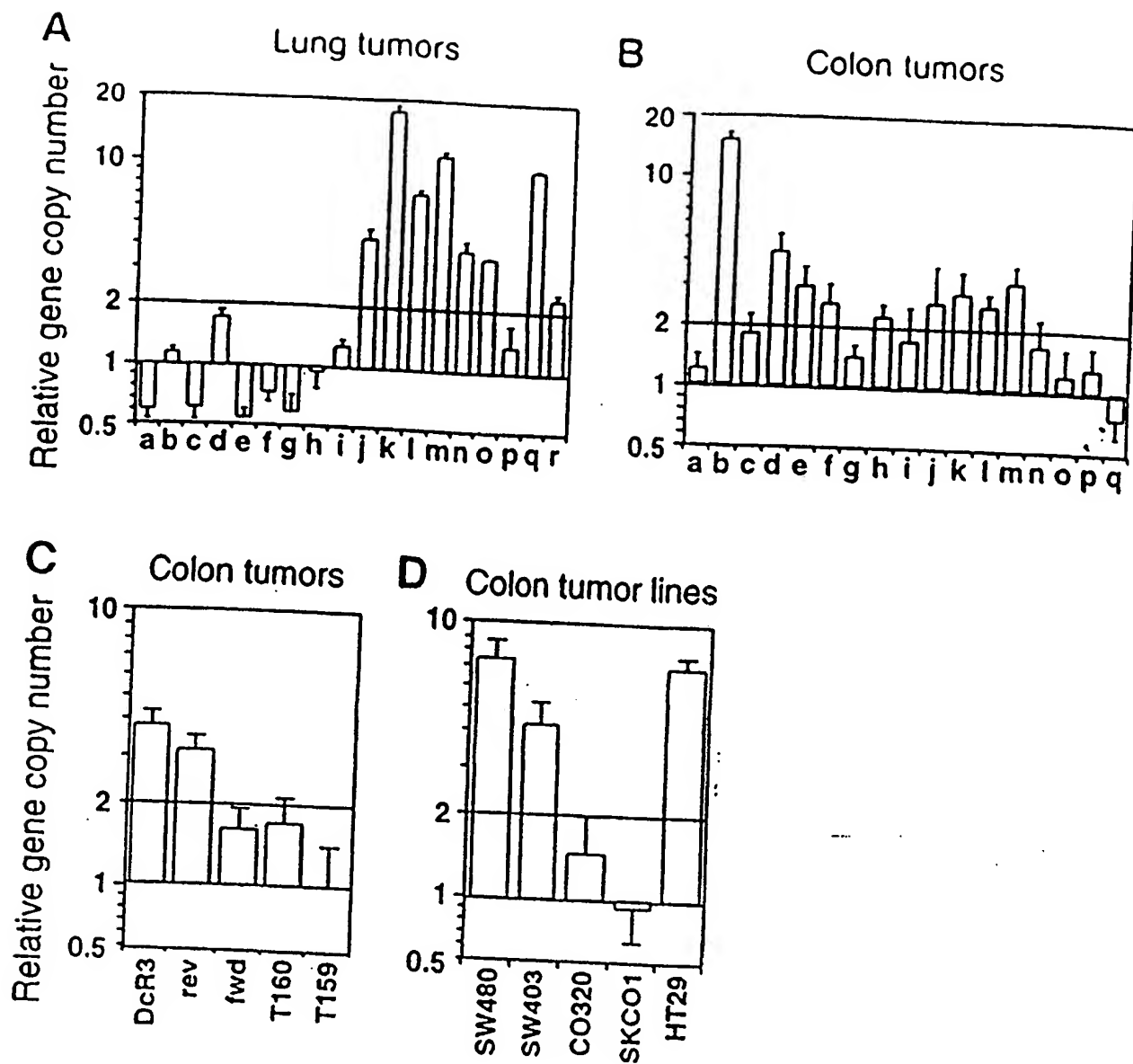


Fig. 10

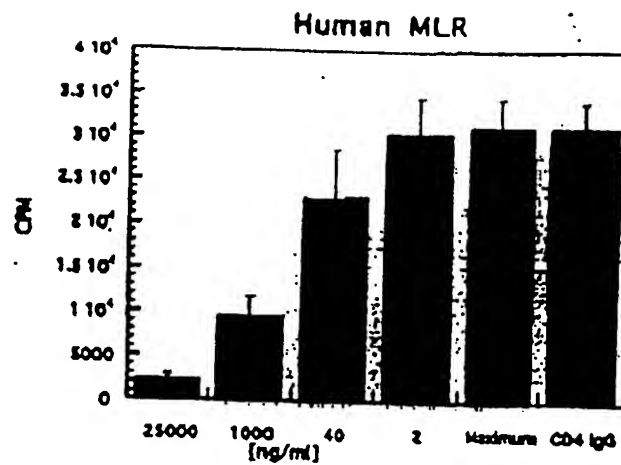


Fig. 11A

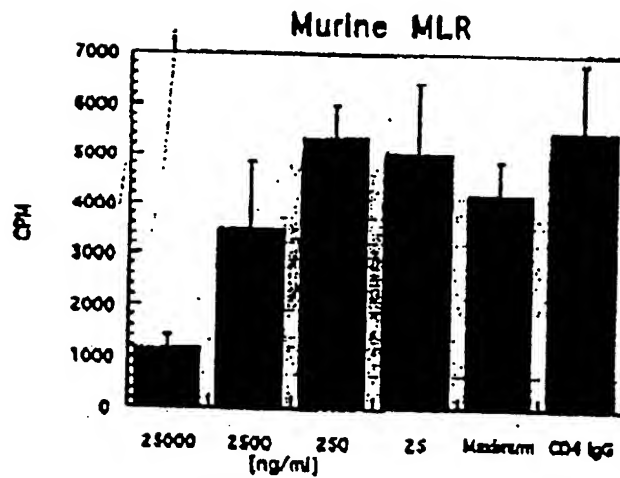


Fig. 11B

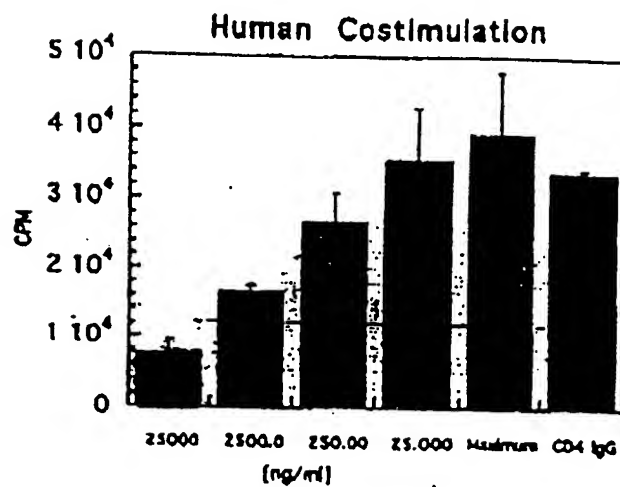


Fig. 11C

FIGURE 12

<u>mAb</u>	<u>Isotype</u>	<u>Antigen Specificity (ELISA)</u>					<u>% Blocking (ELISA)</u>
		<u>DcR3</u>	<u>DR4</u>	<u>DR5</u>	<u>DcR1</u>	<u>OPG</u>	
4B7.1.1	IgG1	+++	-	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.

% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

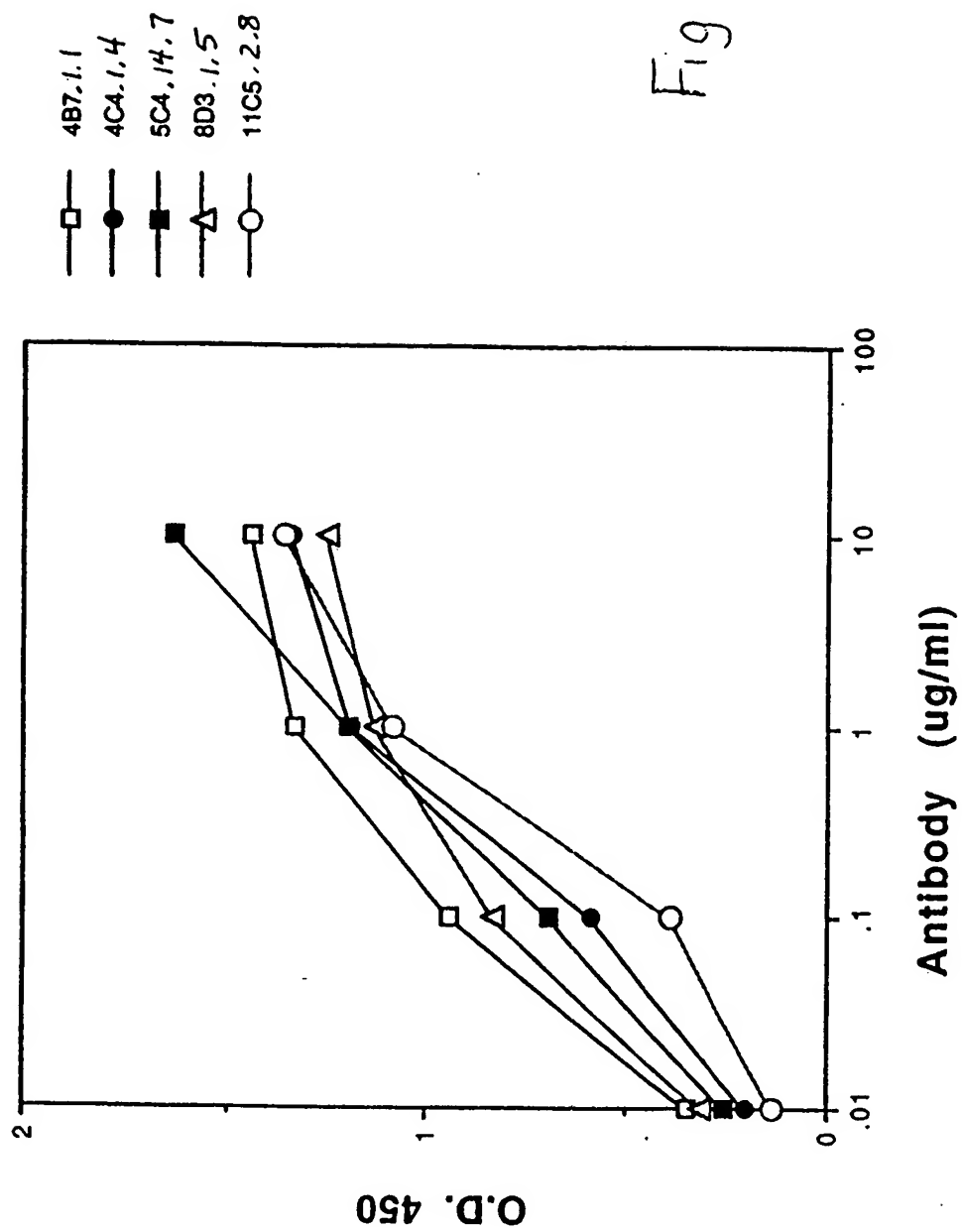


Fig. 13

Fig. 14

